

SEQUENCE LISTING

<110> Kobilka, Brian K.
Ghanouni, Pejman
Lee, Tae Weon

<120> Conformational assays to detect binding
to membrane spanning, signal-transducing proteins

<130> STAN-213CIP

<140> Unassigned
<141> 2003-10-22

<150> PCT/US02/13250
<151> 2002-04-24

<150> 09/935,061
<151> 2001-08-21

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1		5						10				15				

agc	cat	gct	ccg	gac	cac	gac	gtc	acg	cag	caa	agg	gac	gag	gtg	tgg	96
Ser	His	Ala	Pro	Asp	His	Asp	Val	Thr	Gln	Gln	Arg	Asp	Glu	Val	Trp	
20			25						30							

gtg	gtg	ggc	atg	ggc	atc	gtc	atg	tct	ctc	atc	gtc	ctg	gcc	atc	gtg	144
Val	Val	Gly	Met	Gly	Ile	Val	Met	Ser	Leu	Ile	Val	Leu	Ala	Ile	Val	
35			40						45							

ttt	ggc	aat	gtg	ctg	gtc	atc	aca	gcc	att	gcc	aag	ttc	gag	cgt	ctg	192
Phe	Gly	Asn	Val	Leu	Val	Ile	Thr	Ala	Ile	Ala	Lys	Phe	Glu	Arg	Leu	
50			55					60								

cag	acg	gtc	acc	aac	tac	ttc	atc	act	tca	ctg	gcc	tgt	gct	gat	ctg	240
Gln	Thr	Val	Thr	Asn	Tyr	Phe	Ile	Thr	Ser	Leu	Ala	Cys	Ala	Asp	Leu	
65			70						75			80				

gtc	atg	ggc	ctg	gca	gtg	gtg	ccc	ttt	ggg	gcc	gcc	cat	att	ctt	atg	288
Val	Met	Gly	Leu	Ala	Val	Val	Pro	Phe	Gly	Ala	Ala	His	Ile	Leu	Met	
85			90						95							

aaa	atg	tgg	act	ttt	ggc	aac	ttc	tgg	tgc	gag	ttt	tgg	act	tcc	att	336
Lys	Met	Trp	Thr	Phe	Gly	Asn	Phe	Trp	Cys	Glu	Phe	Trp	Thr	Ser	Ile	
100				105						110						

gat	gtg	ctg	tgc	gtc	acg	gct	agc	att	gag	acc	ctg	tgc	gtg	atc	gca	384
Asp	Val	Leu	Cys	Val	Thr	Ala	Ser	Ile	Glu	Thr	Leu	Cys	Val	Ile	Ala	
115			120						125							

gtg gat cgc tac ttt gcc att act tca cct ttc aag tac cag agc ctg Val Asp Arg Tyr Phe Ala Ile Thr Ser Pro Phe Lys Tyr Gln Ser Leu 130 135 140	432
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tca ggc ctt acc tcc ttc ttg ccc att cag atg cac tgg tac cggtt Ser Gly Leu Thr Ser Phe Leu Pro Ile Gln Met His Trp Tyr Arg Ala 165 170 175	528
acc cac cag gaa gcc atc aac tgc tat gcc aat gag acc tgc tgc gac Thr His Gln Glu Ala Ile Asn Cys Tyr Ala Asn Glu Thr Cys Cys Asp 180 185 190	576
ttc ttc acg aac caa gcc tat gcc att gcc tct tcc atc gtg tcc ttc Phe Phe Thr Asn Gln Ala Tyr Ala Ile Ala Ser Ser Ile Val Ser Phe 195 200 205	624
tac gtt ccc ctg gtg atc atg gtc ttc gtc tac tcc agg gtc ttt cag Tyr Val Pro Leu Val Ile Met Val Phe Val Tyr Ser Arg Val Phe Gln 210 215 220	672
gag gcc aaa agg cag ctc cag aag att gac aaa tct gag ggc cgc ttc Glu Ala Lys Arg Gln Leu Gln Lys Ile Asp Lys Ser Glu Gly Arg Phe 225 230 235 240	720
cat gtc cag aac ctt agc cag gtg gag cag gat ggg cgg acg ggg cat His Val Gln Asn Leu Ser Gln Val Glu Gln Asp Gly Arg Thr Gly His 245 250 255	768
gga ctc cgc aga tct tcc aag ttc tgc ttg aag gag cac aaa gcc ctc Gly Leu Arg Arg Ser Ser Lys Phe Cys Leu Lys Glu His Lys Ala Leu 260 265 270	816
aag acg tta ggc atc atc atg ggc act ttc acc ctc tgc tgg ctg ccc Lys Thr Leu Gly Ile Ile Met Gly Thr Phe Thr Leu Cys Trp Leu Pro 275 280 285	864
ttc ttc atc aac att gtg cat gtg atc cag gat aac ctc atc cgt Phe Phe Ile Val Asn Ile Val His Val Ile Gln Asp Asn Leu Ile Arg 290 295 300	912
aag gaa gtt tac atc ctc cta aat tgg ata ggc tat gtc aat tct ggt Lys Glu Val Tyr Ile Leu Leu Asn Trp Ile Gly Tyr Val Asn Ser Gly 305 310 315 320	960
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cag gag ctc ctg tgc ctg cgc agg tct tct ttg aag gcc tat ggg aat Gln Glu Leu Leu Cys Leu Arg Arg Ser Ser Leu Lys Ala Tyr Gly Asn 340 345 350	1056
ggc tac tcc agc aac ggc aac aca ggg gag cag agt gga tat cac gtg Gly Tyr Ser Ser Asn Gly Asn Thr Gly Glu Gln Ser Gly Tyr His Val 355 360 365	1104

gaa cag gag aaa gaa aat aaa ctg ctg tgt gaa gac ctc cca ggc acg Glu Gln Glu Lys Glu Asn Lys Leu Leu Cys Glu Asp Leu Pro Gly Thr 370 375 380	1152
gaa gac ttt gtg ggc cat caa ggt act gtg cct agc gat aac att gat Glu Asp Phe Val Gly His Gln Gly Thr Val Pro Ser Asp Asn Ile Asp 385 390 395 400	1200
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Val Val Gly Met Gly Ile Val Met Ser Leu Ile Val Leu Ala Ile Val 35 40 45	
Phe Gly Asn Val Leu Val Ile Thr Ala Ile Ala Lys Phe Glu Arg Leu 50 55 60	
Gln Thr Val Thr Asn Tyr Phe Ile Thr Ser Leu Ala Cys Ala Asp Leu 65 70 75 80	
Val Met Gly Leu Ala Val Val Pro Phe Gly Ala Ala His Ile Leu Met 85 90 95	
Lys Met Trp Thr Phe Gly Asn Phe Trp Cys Glu Phe Trp Thr Ser Ile 100 105 110	
Asp Val Leu Cys Val Thr Ala Ser Ile Glu Thr Leu Cys Val Ile Ala 115 120 125	
Val Asp Arg Tyr Phe Ala Ile Thr Ser Pro Phe Lys Tyr Gln Ser Leu 130 135 140	
Leu Thr Lys Asn Lys Ala Arg Val Ile Ile Leu Met Val Trp Ile Val 145 150 155 160	
Ser Gly Leu Thr Ser Phe Leu Pro Ile Gln Met His Trp Tyr Arg Ala 165 170 175	
Thr His Gln Glu Ala Ile Asn Cys Tyr Ala Asn Glu Thr Cys Cys Asp 180 185 190	
Phe Phe Thr Asn Gln Ala Tyr Ala Ile Ala Ser Ser Ile Val Ser Phe 195 200 205	
Tyr Val Pro Leu Val Ile Met Val Phe Val Tyr Ser Arg Val Phe Gln 210 215 220	
Glu Ala Lys Arg Gln Leu Gln Lys Ile Asp Lys Ser Glu Gly Arg Phe 225 230 235 240	
His Val Gln Asn Leu Ser Gln Val Glu Gln Asp Gly Arg Thr Gly His 245 250 255	
Gly Leu Arg Arg Ser Ser Lys Phe Cys Leu Lys Glu His Lys Ala Leu 260 265 270	
Lys Thr Leu Gly Ile Ile Met Gly Thr Phe Thr Leu Cys Trp Leu Pro 275 280 285	
Phe Phe Ile Val Asn Ile Val His Val Ile Gln Asp Asn Leu Ile Arg 290 295 300	
Lys Glu Val Tyr Ile Leu Leu Asn Trp Ile Gly Tyr Val Asn Ser Gly	

305	310	315	320
Phe Asn Pro Leu Ile Tyr Cys Arg Ser	Pro Asp Phe Arg Ile Ala Phe		
325	330	335	
Gln Glu Leu Leu Cys Leu Arg Arg Ser	Ser Leu Lys Ala Tyr Gly Asn		
340	345	350	
Gly Tyr Ser Ser Asn Gly Asn Thr Gly Glu Gln Ser Gly Tyr His Val			
355	360	365	
Glu Gln Glu Lys Glu Asn Lys Leu Leu Cys Glu Asp Leu Pro Gly Thr			
370	375	380	
Glu Asp Phe Val Gly His Gln Gly Thr Val Pro Ser Asp Asn Ile Asp			
385	390	395	400
Ser Gln Gly Arg Asn Cys Ser Thr Asn Asp Ser Leu Leu			
405	410		

<210> 7

<211> 1239

<212> DNA

<213> Artificial Sequence

<220>

<223> Beta-2 Adrenergic Receptor with TEV site in 2nd
intracellular loop

<221> CDS

<222> (1)...(1239)

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Met Gly Gln Pro Gly Asn Gly Ser Ala Phe Leu Leu Ala Pro Asn Arg			
1	5	10	15

agc cat gcg ccg gac cac gac gtc acg cag caa agg gac gag gtg tgg	96		
Ser His Ala Pro Asp His Asp Val Thr Gln Gln Arg Asp Glu Val Trp			
20	25	30	

gtg gtg ggc atg ggc atc gtc atg tct ctc atc gtc ctg gcc atc gtg	144		
Val Val Gly Met Gly Ile Val Met Ser Leu Ile Val Leu Ala Ile Val			
35	40	45	

ttt ggc aat gtg ctg gtc atc aca gcc att gcc aag ttc gag cgt ctg	192		
Phe Gly Asn Val Leu Val Ile Thr Ala Ile Ala Lys Phe Glu Arg Leu			
50	55	60	

cag acg gtc acc aac tac ttc atc act tca ctg gcc tgt gct gat ctg	240		
Gln Thr Val Thr Asn Tyr Phe Ile Thr Ser Leu Ala Cys Ala Asp Leu			
65	70	75	80

gtc atg ggc ctg gca gtg gtg ccc ttt ggg gcc gcc cat att ctt atg	288		
Val Met Gly Leu Ala Val Val Pro Phe Gly Ala Ala His Ile Leu Met			
85	90	95	

aaa atg tgg act ttt ggc aac ttc tgg tgc gag ttt tgg act tcc att	336		
Lys Met Trp Thr Phe Gly Asn Phe Trp Cys Glu Phe Trp Thr Ser Ile			
100	105	110	

gat gtg ctg tgc gtc acg gct agc att gag acc ctg tgc gtg atc gca	384		
Asp Val Leu Cys Val Thr Ala Ser Ile Glu Thr Leu Cys Val Ile Ala			
115	120	125	

gtg gat cgc tac ttt gcc att act tca cct ttc aag tac cag agc ctg Val Asp Arg Tyr Phe Ala Ile Thr Ser Pro Phe Lys Tyr Gln Ser Leu 130 135 140	432
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tca ggc ctt acc tcc ttc ttg ccc att cag atg cac tgg tac cgg gcc Ser Gly Leu Thr Ser Phe Leu Pro Ile Gln Met His Trp Tyr Arg Ala 165 170 175	528
acc cac cag gaa gcc atc aac tgc tat gcc aat gag acc tgc tgt gac Thr His Gln Glu Ala Ile Asn Cys Tyr Ala Asn Glu Thr Cys Cys Asp 180 185 190	576
ttc ttc acg aac caa gcc tat gcc att gcc tct tcc atc gtg tcc ttc Phe Phe Thr Asn Gln Ala Tyr Ala Ile Ala Ser Ser Ile Val Ser Phe 195 200 205	624
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cat gtc cag aac ctt agc cag gtg gag cag gat ggg cgg acg ggg cat His Val Gln Asn Leu Ser Gln Val Glu Gln Asp Gly Arg Thr Gly His 245 250 255	768
gga ctc gaa aac ctc tac ttc cag ggg ttg aag gag cac aaa gcc ctc Gly Leu Glu Asn Leu Tyr Phe Gln Gly Leu Lys Glu His Lys Ala Leu 260 265 270	816
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aag gaa gtt tac atc ctc cta aat tgg ata ggc tat gtc aat tct ggt Lys Glu Val Tyr Ile Leu Leu Asn Trp Ile Gly Tyr Val Asn Ser Gly 305 310 315 320	960
ttc aat ccc ctt atc tac tgc cgg agc cca gat ttc agg att gcc ttc Phe Asn Pro Leu Ile Tyr Cys Arg Ser Pro Asp Phe Arg Ile Ala Phe 325 330 335	1008
cag gag ctc ctg tgc ctc cgc agg tct ttg aag gcc tat ggg aat Gln Glu Leu Leu Cys Leu Arg Arg Ser Ser Leu Lys Ala Tyr Gly Asn 340 345 350	1056
ggc tac tcc agc aac ggc aac aca ggg gag cag agt gga tat cac gtg Gly Tyr Ser Ser Asn Gly Asn Thr Gly Glu Gln Ser Gly Tyr His Val 355 360 365	1104

gaa cag gag aaa gaa aat aaa ctg ctg tgc gaa gac ctc cca ggc acg . . . 1152
Glu Gln Glu Lys Glu Asn Lys Leu Leu Cys Glu Asp Leu Pro Gly Thr
370 . . . 375 . . . 380

gaa gac ttt gtg ggc cat caa ggt act gtg cct agc gat aac att gat . . . 1200
Glu Asp Phe Val Gly His Gln Gly Thr Val Pro Ser Asp Asn Ile Asp
385 . . . 390 . . . 395 . . . 400

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405 . . . 410

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<211> 413

<212> PRT

<213> Artificial Sequence

<220>

<223> Beta-2 Adrenergic Receptor with TEV site in 2nd
intracellular loop

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20 . . . 25 . . . 30

Val Val Gly Met Gly Ile Val Met Ser Leu Ile Val Leu Ala Ile Val
35 . . . 40 . . . 45

Phe Gly Asn Val Leu Val Ile Thr Ala Ile Ala Lys Phe Glu Arg Leu
50 . . . 55 . . . 60

Gln Thr Val Thr Asn Tyr Phe Ile Thr Ser Leu Ala Cys Ala Asp Leu
65 . . . 70 . . . 75 . . . 80

Val Met Gly Leu Ala Val Val Pro Phe Gly Ala Ala His Ile Leu Met
85 . . . 90 . . . 95

Lys Met Trp Thr Phe Gly Asn Phe Trp Cys Glu Phe Trp Thr Ser Ile
100 . . . 105 . . . 110

Asp Val Leu Cys Val Thr Ala Ser Ile Glu Thr Leu Cys Val Ile Ala
115 . . . 120 . . . 125

Val Asp Arg Tyr Phe Ala Ile Thr Ser Pro Phe Lys Tyr Gln Ser Leu
130 . . . 135 . . . 140

Leu Thr Lys Asn Lys Ala Arg Val Ile Ile Leu Met Val Trp Ile Val
145 . . . 150 . . . 155 . . . 160

Ser Gly Leu Thr Ser Phe Leu Pro Ile Gln Met His Trp Tyr Arg Ala
165 . . . 170 . . . 175

Thr His Gln Glu Ala Ile Asn Cys Tyr Ala Asn Glu Thr Cys Cys Asp
180 . . . 185 . . . 190

Phe Phe Thr Asn Gln Ala Tyr Ala Ile Ala Ser Ser Ile Val Ser Phe
195 . . . 200 . . . 205

Tyr Val Pro Leu Val Ile Met Val Phe Val Tyr Ser Arg Val Phe Gln
210 . . . 215 . . . 220

Glu Ala Lys Arg Gln Leu Gln Lys Ile Asp Lys Ser Glu Gly Arg Phe
225 . . . 230 . . . 235 . . . 240

His Val Gln Asn Leu Ser Gln Val Glu Gln Asp Gly Arg Thr Gly His
245 . . . 250 . . . 255

Gly Leu Glu Asn Leu Tyr Phe Gln Gly Leu Lys Glu His Lys Ala Leu
260 . . . 265 . . . 270

Lys Thr Leu Gly Ile Ile Met Gly Thr Phe Thr Leu Cys Trp Leu Pro

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Phe Phe Ile Val Asn Ile Val His Val Ile Gln Asp Asn Leu	Ile Arg		
290	295	300	
Lys Glu Val Tyr Ile Leu Leu Asn Trp Ile Gly Tyr Val Asn Ser Gly			
305	310	315	320
Phe Asn Pro Leu Ile Tyr Cys Arg Ser Pro Asp Phe Arg Ile Ala Phe			
325	330	335	
Gln Glu Leu Leu Cys Leu Arg Arg Ser Ser Leu Lys Ala Tyr Gly Asn			
340	345	350	
Gly Tyr Ser Ser Asn Gly Asn Thr Gly Glu Gln Ser Gly Tyr His Val			
355	360	365	
Glu Gln Glu Lys Glu Asn Lys Leu Leu Cys Glu Asp Leu Pro Gly Thr			
370	375	380	
Glu Asp Phe Val Gly His Gln Gly Thr Val Pro Ser Asp Asn Ile Asp			
385	390	395	400
Ser Gln Gly Arg Asn Cys Ser Thr Asn Asp Ser Leu Leu			
405	410		

<210> 9

<211> 1251

<212> DNA

<213> Artificial Sequence

<220>

<223> Beta-2 Adrenergic Receptor with TEV site in 3rd intracellular loop

<221> CDS

<222> (1)...(1251)

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1 5 10 15

48

agc cat gcg ccg gac cac gac gtc acg cag caa agg gac gag gtg tgg
Ser His Ala Pro Asp His Asp Val Thr Gln Gln Arg Asp Glu Val Trp
20 25 30

96

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gtg gtg ggc atg ggc atc gtc atg tct ctc atc gtc ctg gcc atc gtg
Val Val Gly Met Gly Ile Val Met Ser Leu Ile Val Leu Ala Ile Val
. 35 40 45

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144

ttt ggc aat gtg ctg gtc atc aca gcc att gcc aag ttc gag cgt ctg
Phe Gly Asn Val Leu Val Ile Thr Ala Ile Ala Lys Phe Glu Arg Leu
50 55 60

192

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cag acg gtc acc aac tac ttc atc act tca ctg gcc tgt gct gat ctg
Gln Thr Val Thr Asn Tyr Phe Ile Thr Ser Leu Ala Cys Ala Asp Leu
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240

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Val Met Gly Leu Ala Val Val Pro Phe Gly Ala Ala His Ile Leu Met
          85          90          95

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288

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aaa atg tgg act ttt ggc aac ttc tgg tgc gag ttt tgg act tcc att
Lys Met Trp Thr Phe Gly Asn Phe Trp Cys Glu Phe Trp Thr Ser Ile
100          105          110

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336

gat gtg ctg tgc gtc acg gct agc att gag acc ctg tgc gtg atc gca Asp Val Leu Cys Val Thr Ala Ser Ile Glu Thr Leu Cys Val Ile Ala 115 120 125	384
gtg gat cgc tac ttt gcc att act tca cct ttc aag gag aat ctc tac Val Asp Arg Tyr Phe Ala Ile Thr Ser Pro Phe Lys Glu Asn Leu-Tyr 130 135 140	432
ttc cag ggc ctg ctg acc aag aat aag gcc cggtc att ctg atg Phe Gln Gly Leu Leu Thr Lys Asn Lys Ala Arg Val Ile Ile Leu Met 145 150 155 160	480
gtg tgg att gtg tca ggc ctt acc tcc ttc ttg ccc att cag atg cac Val Trp Ile Val Ser Gly Leu Thr Ser Phe Leu Pro Ile Gln Met His 165 170 175	528
tgg tac cgg gcc acc cac cag gaa gcc atc aac tgc tat gcc aat gag Trp Tyr Arg Ala Thr His Gln Glu Ala Ile Asn Cys Tyr Ala Asn Glu 180 185 190	576
acc tgc tgt gac ttc ttc acg aac caa gcc tat gcc att gcc tct tcc Thr Cys Cys Asp Phe Phe Thr Asn Gln Ala Tyr Ala Ile Ala Ser Ser 195 200 205	624
atc gtg tcc ttc tac gtt ccc ctg gtg atc atg gtc ttc gtc tac tcc Ile Val Ser Phe Tyr Val Pro Leu Val Ile Met Val Phe Val Tyr Ser 210 215 220	672
agg gtc ttt cag gag gcc aaa agg cag ctc cag aag att gac aaa tct Arg Val Phe Gln Glu Ala Lys Arg Gln Leu Gln Lys Ile Asp Lys Ser 225 230 235 240	720
gag ggc cgc ttc cat gtc cag aac ctt agc cag gtg gag cag gat ggg Glu Gly Arg Phe His Val Gln Asn Leu Ser Gln Val Glu Gln Asp Gly 245 250 255	768
cgg acg ggg cat gga ctc cgc aga tct tcc aag ttc tgc ttg aag gag Arg Thr Gly His Gly Leu Arg Arg Ser Ser Lys Phe Cys Leu Lys Glu 260 265 270	816
cac aaa gcc ctc aag acg tta ggc atc atc atg ggc act ttc acc ctc His Lys Ala Leu Lys Thr Leu Gly Ile Ile Met Gly Thr Phe Thr Leu 275 280 285	864
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aac ctc atc cgt aag gaa gtt tac atc ctc cta aat tgg ata ggc tat Asn Leu Ile Arg Lys Glu Val Tyr Ile Leu Leu Asn Trp Ile Gly Tyr 305 310 315 320	960
gtc aat tct ggt ttc aat ccc ctt atc tac tgc cgg agc cca gat ttc Val Asn Ser Gly Phe Asn Pro Leu Ile Tyr Cys Arg Ser Pro Asp Phe 325 330 335	1008
agg att gcc ttc cag gag ctc ctg tgc ctg cgc agg tct ttc ttg aag Arg Ile Ala Phe Gln Glu Leu Leu Cys Leu Arg Arg Ser Ser Leu Lys 340 345 350	1056

gcc tat ggg aat ggc tac tcc	agc aac ggc aac aca	ggg gag cag agt	1104
Ala Tyr Gly Asn Gly Tyr Ser	Ser Asn Gly Asn Thr	Gly Glu Gln Ser	
355	360	365	
gga tat cac gtg gaa cag gag	aaa gaa aat aaa	ctg ctg tgt gaa gac	1152
Gly Tyr His Val Glu Gln	Glu Lys Glu Asn Lys	Leu Leu Cys Glu Asp	
370	375	380	
ctc cca ggc acg gaa gac ttt	gtg ggc cat caa ggt	act gtg cct agc	1200
Leu Pro Gly Thr Glu Asp	Phe Val Gly His	Gln Gly Thr Val Pro Ser	
385	390	395	400
gat aac att gat tca caa ggg	agg aat tgt agt aca	aat gac tca ctg	1248
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405	410	415	
ctg			1251
Leu			

<210> 10

<211> 417

<212> PRT

<213> Artificial Sequence

<220>

<223> Beta-2 Adrenergic Receptor with TEV site in 3rd
intracellular loop

<400> 10

Met Gly Gln Pro Gly Asn Gly Ser Ala Phe	Leu Leu Ala Pro Asn Arg		
1	5	10	15
Ser His Ala Pro Asp His Asp Val Thr	Gln Gln Arg Asp Glu Val Trp		
20	25	30	
Val Val Gly Met Gly Ile Val Met Ser	Leu Ile Val Leu Ala Ile Val		
35	40	45	
Phe Gly Asn Val Leu Val Ile Thr Ala Ile	Ala Lys Phe Glu Arg Leu		
50	55	60	
Gln Thr Val Thr Asn Tyr Phe Ile Thr	Ser Leu Ala Cys Ala Asp Leu		
65	70	75	80
Val Met Gly Leu Ala Val Val Pro Phe	Gly Ala Ala His Ile Leu Met		
85	90	95	
Lys Met Trp Thr Phe Gly Asn Phe Trp	Cys Glu Phe Trp Thr Ser Ile		
100	105	110	
Asp Val Leu Cys Val Thr Ala Ser Ile	Glu Thr Leu Cys Val Ile Ala		
115	120	125	
Val Asp Arg Tyr Phe Ala Ile Thr Ser	Pro Phe Lys Glu Asn Leu Tyr		
130	135	140	
Phe Gln Gly Leu Leu Thr Lys Asn Lys	Ala Arg Val Ile Ile Leu Met		
145	150	155	160
Val Trp Ile Val Ser Gly Leu Thr Ser	Phe Leu Pro Ile Gln Met His		
165	170	175	
Trp Tyr Arg Ala Thr His Gln Glu	Ala Ile Asn Cys Tyr Ala Asn Glu		
180	185	190	
Thr Cys Cys Asp Phe Phe Thr Asn Gln	Ala Tyr Ala Ile Ala Ser Ser		
195	200	205	
Ile Val Ser Phe Tyr Val Pro Leu Val	Ile Met Val Phe Val Tyr Ser		

210	215	220
Arg Val Phe Gln Glu Ala Lys Arg Gln Leu Gln Lys Ile Asp Lys Ser		
225	230	240
Glu Gly Arg Phe His Val Gln Asn Leu Ser Gln Val Glu Gln Asp Gly		
245	250	255
Arg Thr Gly His Gly Leu Arg Arg Ser Ser Lys Phe Cys Leu Lys Glu		
260	265	270
His Lys Ala Leu Lys Thr Leu Gly Ile Ile Met Gly Thr Phe Thr Leu		
275	280	285
Cys Trp Leu Pro Phe Phe Ile Val Asn Ile Val His Val Ile Gln Asp		
290	295	300
Asn Leu Ile Arg Lys Glu Val Tyr Ile Leu Leu Asn Trp Ile Gly Tyr		
305	310	320
Val Asn Ser Gly Phe Asn Pro Leu Ile Tyr Cys Arg Ser Pro Asp Phe		
325	330	335
Arg Ile Ala Phe Gln Glu Leu Leu Cys Leu Arg Arg Ser Ser Leu Lys		
340	345	350
Ala Tyr Gly Asn Gly Tyr Ser Ser Asn Gly Asn Thr Gly Glu Gln Ser		
355	360	365
Gly Tyr His Val Glu Gln Glu Lys Glu Asn Lys Leu Leu Cys Glu Asp		
370	375	380
Leu Pro Gly Thr Glu Asp Phe Val Gly His Gln Gly Thr Val Pro Ser		
385	390	395
Asp Asn Ile Asp Ser Gln Gly Arg Asn Cys Ser Thr Asn Asp Ser Leu		
405	410	415
Leu		

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<220>
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Met Asp Ser Ser Ala Ala Pro Thr Asn Ala Ser Asn Cys Thr Asp Ala			
1	5	10	15
ttg gcg tac tca agt tgc tcc cca gca ccc agc ccc ggt tcc tgg gtc			96
Leu Ala Tyr Ser Ser Cys Ser Pro Ala Pro Ser Pro Gly Ser Trp Val			
20	25	30	
aac ttg tcc cac tta gat ggc gac ctg tcc gac cca tgc ggt ccg aac			144
Asn Leu Ser His Leu Asp Gly Asp Leu Ser Asp Pro Cys Gly Pro Asn			
35	40	45	
cgc acc gac ctg ggc ggg aga gac agc ctg tgc cct cca acc ggc agt			192
Arg Thr Asp Leu Gly Gly Arg Asp Ser Leu Cys Pro Pro Thr Gly Ser			
50	55	60	
ccc tcc atg atc acg gcc atc acg atc atg gcc ctc tac tcc atc gtg			240
Pro Ser Met Ile Thr Ala Ile Thr Ile Met Ala Leu Tyr Ser Ile Val			
65	70	75	80
tgc gtg gtg ggg ctc ttc gga aac ttc ctg gtc atg tat gtg att gtc			288

Cys Val Val Gly Leu Phe Gly Asn Phe Leu Val Met Tyr Val Ile Val	85	90	95	
aga tac acc aag atg aag act gcc acc aac atc tac att ttc aac ctt				336
Arg Tyr Thr Lys Met Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu	100	105	110	
gct ctg gca gat gcc tta gcc acc agt acc ctg ccc ttc cag agt gtg				384
Ala Leu Ala Asp Ala Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Val	115	120	125	
aat tac cta atg gga aca tgg cca ttt gga acc atc ctt tgc aag ata				432
Asn Tyr Leu Met Gly Thr Trp Pro Phe Gly Thr Ile Leu Cys Lys Ile	130	135	140	
gtg atc tcc ata gat tac tat aac atg ttc acc agc ata ttc acc ctc				480
Val Ile Ser Ile Asp Tyr Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu	145	150	155	160
tgc acc atg agt gtt gat cga tac att gca gtc tgc cac cct gtc aag				528
Cys Thr Met Ser Val Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys	165	170	175	
gcc tta gat ttc cgt act ccc cga aat gcc aaa att atc aat gtc tgc				576
Ala Leu Asp Phe Arg Thr Pro Arg Asn Ala Lys Ile Ile Asn Val Cys	180	185	190	
aac tgg atc ctc tct tca gcc att ggt ctt cct gta atg ttc ata gct				624
Asn Trp Ile Leu Ser Ser Ala Ile Gly Leu Pro Val Met Phe Ile Ala	195	200	205	
aca aca aaa tac agg caa ggt tcc ata gat tgt aca cta aca ttc tct				672
Thr Thr Lys Tyr Arg Gln Gly Ser Ile Asp Cys Thr Leu Thr Phe Ser	210	215	220	
cat cca acc tgg tac tgg gaa aac ctg ctg aag atc tgt gtt ttc atc				720
His Pro Thr Trp Tyr Trp Glu Asn Leu Leu Lys Ile Cys Val Phe Ile	225	230	235	240
ttc gcc ttc att atg cca gtg ctc atc att acc gtg tgc tat gga ctg				768
Phe Ala Phe Ile Met Pro Val Leu Ile Ile Thr Val Cys Tyr Gly Leu	245	250	255	
atg atc ttg cgc ctc aag agt gtc cgc atg ctc tct ggc tcc aaa gaa				816
Met Ile Leu Arg Leu Lys Ser Val Arg Met Leu Ser Gly Ser Lys Glu	260	265	270	
aag gac agg aat ctt cga agg atc acc agg atg gtg ctg gtg gtg gtg				864
Lys Asp Arg Asn Leu Arg Arg Ile Thr Arg Met Val Leu Val Val Val	275	280	285	
gct gtg ttc atc gtc tgc tgg act ccc att cac att tac gtc atc att				912
Ala Val Phe Ile Val Cys Trp Thr Pro Ile His Ile Tyr Val Ile Ile	290	295	300	
aaa gcc ttg gtt aca atc cca gaa act acg ttc cag act gtt tct tgg				960
Lys Ala Leu Val Thr Ile Pro Glu Thr Thr Phe Gln Thr Val Ser Trp	305	310	315	320

cac ttc tgc att gct cta ggt tac aca aac agc tgc ctc aac cca gtc His Phe Cys Ile Ala Leu Gly Tyr Thr Asn Ser Cys Leu Asn Pro Val 325 330 335	1008																																																																
ctt tat gca ttt ctg gat gaa aac ttc aaa cga tgc ttc aga gag ttc Leu Tyr Ala Phe Leu Asp Glu Asn Phe Lys Arg Cys Phe Arg Glu Phe 340 345 350	1056																																																																
tgt atc cca acc tct tcc aac att gag caa caa aac tcc act cga att Cys Ile Pro Thr Ser Ser Asn Ile Glu Gln Gln Asn Ser Thr Arg Ile 355 360 365	1104																																																																
cgt cag aac act aga gac cac ccc tcc acg gcc aat aca gtg gat aga Arg Gln Asn Thr Arg Asp His Pro Ser Thr Ala Asn Thr Val Asp Arg 370 375 380	1152																																																																
act aat cat cag gta cgc agt ctc Thr Asn His Gln Val Arg Ser Leu 385 390	1176																																																																
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Met Asp Ser Ser Ala Ala Pro Thr Asn Ala Ser Asn Cys Thr Asp Ala																																																																	
1 5 10 15																																																																	
Leu Ala Tyr Ser Ser Cys Ser Pro Ala Pro Ser Pro Gly Ser Trp Val																																																																	
20 25 30																																																																	
Asn Leu Ser His Leu Asp Gly Asp Leu Ser Asp Pro Cys Gly Pro Asn																																																																	
35 40 45																																																																	
Arg Thr Asp Leu Gly Gly Arg Asp Ser Leu Cys Pro Pro Thr Gly Ser																																																																	
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65 70 75 80																																																																	
Cys Val Val Gly Leu Phe Gly Asn Phe Leu Val Met Tyr Val Ile Val																																																																	
85 90 95																																																																	
Arg Tyr Thr Lys Met Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu																																																																	
100 105 110																																																																	
Ala Leu Ala Asp Ala Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Val																																																																	
115 120 125																																																																	
Asn Tyr Leu Met Gly Thr Trp Pro Phe Gly Thr Ile Leu Cys Lys Ile																																																																	
130 135 140																																																																	
Val Ile Ser Ile Asp Tyr Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu																																																																	
145 150 155 160																																																																	
Cys Thr Met Ser Val Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys																																																																	
165 170 175																																																																	
Ala Leu Asp Phe Arg Thr Pro Arg Asn Ala Lys Ile Ile Asn Val Cys																																																																	
180 185 190																																																																	
Asn Trp Ile Leu Ser Ser Ala Ile Gly Leu Pro Val Met Phe Ile Ala																																																																	
195 200 205																																																																	
Thr Thr Lys Tyr Arg Gln Gly Ser Ile Asp Cys Thr Leu Thr Phe Ser																																																																	
210 215 220																																																																	
His Pro Thr Trp Tyr Trp Glu Asn Leu Leu Lys Ile Cys Val Phe Ile																																																																	
225 230 235 240																																																																	
Phe Ala Phe Ile Met Pro Val Leu Ile Ile Thr Val Cys Tyr Gly Leu																																																																	
245 250 255																																																																	

Met Ile Leu Arg Leu Lys Ser Val Arg Met Leu Ser Gly Ser Lys Glu
 260 265 270
 Lys Asp Arg Asn Leu Arg Arg Ile Thr Arg Met Val Leu Val Val Val
 275 280 285
 Ala Val Phe Ile Val Cys Trp Thr Pro Ile His Ile Tyr Val Ile Ile
 290 295 300
 Lys Ala Leu Val Thr Ile Pro Glu Thr Thr Phe Gln Thr Val Ser Trp
 305 310 315 320
 His Phe Cys Ile Ala Leu Gly Tyr Thr Asn Ser Cys Leu Asn Pro Val
 325 330 335
 Leu Tyr Ala Phe Leu Asp Glu Asn Phe Lys Arg Cys Phe Arg Glu Phe
 340 345 350
 Cys Ile Pro Thr Ser Ser Asn Ile Glu Gln Gln Asn Ser Thr Arg Ile
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<210> 13

<211> 1176

<212> DNA

<213> Artificial Sequence

<220>

<223> ' Opioid receptor with TEV site in 2nd
intracellular loop

<221> CDS

<222> (1)...(1176)

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atg gac agc agc gct gcc ccc acg aac gcc agc aat tgc act gat gcc
Met Asp Ser Ser Ala Ala Pro Thr Asn Ala Ser Asn Cys Thr Asp Ala
1 5 10 15

48

ttg gcg tac tca agt tgc tcc cca gca ccc agc ccc ggt tcc tgg gtc
Leu Ala Tyr Ser Ser Cys Ser Pro Ala Pro Ser Pro Gly Ser Trp Val
20 25 30

96

aac ttg tcc cac tta gat ggc gac ctg tcc gac cca tgc ggt ccg aac
Asn Leu Ser His Leu Asp Gly Asp Leu Ser Asp Pro Cys Gly Pro Asn
35 40 45

144

cgc acc gac ctg ggc ggg aga gac agc ctg tgc cct cca acc ggc agt
Arg Thr Asp Leu Gly Gly Arg Asp Ser Leu Cys Pro Pro Thr Gly Ser
50 55 60

192

ccc tcc atg atc acg gcc atc acg atc atg gcc ctc tac tcc atc gtg
Pro Ser Met Ile Thr Ala Ile Thr Ile Met Ala Leu Tyr Ser Ile Val
65 70 75 80

240

tgc gtg gtg ggg ctc ttc gga aac ttc ctg gtc atg tat gtg att gtc
Cys Val Val Gly Leu Phe Gly Asn Phe Leu Val Met Tyr Val Ile Val
85 90 95

288

aga tac acc aag atg aag act gcc acc aac atc tac att ttc aac ctt
Arg Tyr Thr Lys Met Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu
100 105 110

336

gct ctg gca gat gcc tta gcc acc agt acc ctg ccc ttc cag agt gtg Ala Leu Ala Asp Ala Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Val 115 120 125	384
aat tac cta atg gga aca tgg cca ttt gga acc atc ctt tgc aag ata Asn Tyr Leu Met Gly Thr Trp Pro Phe Gly Thr Ile Leu Cys Lys Ile 130 135 140	432
gtg atc tcc ata gat tac tat aac atg ttc acc agc ata ttc acc ctc Val Ile Ser Ile Asp Tyr Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu 145 150 155 160	480
tgc acc atg agt gtt gat cga tac att gca gtc tgc cac cct gtc aag Cys Thr Met Ser Val Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys 165 170 175	528
gaa aac ctc tac ttc cag ggg cga aat gcc aaa att atc aat gtc tgc Glu Asn Leu Tyr Phe Gln Gly Arg Asn Ala Lys Ile Ile Asn Val Cys 180 185 190	576
aac tgg atc ctc tct tca gcc att ggt ctt cct gta atg ttc ata gct Asn Trp Ile Leu Ser Ser Ala Ile Gly Leu Pro Val Met Phe Ile Ala 195 200 205	624
aca aca aaa tac agg caa ggt tcc ata gat tgt aca cta aca ttc tct Thr Thr Lys Tyr Arg Gln Gly Ser Ile Asp Cys Thr Leu Thr Phe Ser 210 215 220	672
cat cca acc tgg tac tgg gaa aac ctg ctg aag atc tgt gtt ttc atc His Pro Thr Trp Tyr Trp Glu Asn Leu Leu Lys Ile Cys Val Phe Ile 225 230 235 240	720
ttc gcc ttc att atg cca gtg ctc atc att acc gtg tgc tat gga ctg Phe Ala Phe Ile Met Pro Val Leu Ile Ile Thr Val Cys Tyr Gly Leu 245 250 255	768
atg atc ttg cgc ctc aag agt gtc cgc atg ctc tct ggc tcc aaa gaa Met Ile Leu Arg Leu Lys Ser Val Arg Met Leu Ser Gly Ser Lys Glu 260 265 270	816
aag gac agg aat ctt cga agg atc acc agg atg gtg ctg gtg gtg gtg Lys Asp Arg Asn Leu Arg Arg Ile Thr Arg Met Val Leu Val Val Val 275 280 285	864
gct gtg ttc atc gtc tgc tgg act ccc att cac att tac gtc atc att Ala Val Phe Ile Val Cys Trp Thr Pro Ile His Ile Tyr Val Ile Ile 290 295 300	912
aaa gcc ttg gtt aca atc cca gaa act acg ttc cag act gtt tct tgg Lys Ala Leu Val Thr Ile Pro Glu Thr Thr Phe Gln Thr Val Ser Trp 305 310 315 320	960
cac ttc tgc att gct cta ggt tac aca aac agc tgc ctc aac cca gtc His Phe Cys Ile Ala Leu Gly Tyr Thr Asn Ser Cys Leu Asn Pro Val 325 330 335	1008
ctt tat gca ttt ctg gat gaa aac ttc aaa cga tgc ttc aga gag ttc Leu Tyr Ala Phe Leu Asp Glu Asn Phe Lys Arg Cys Phe Arg Glu Phe	1056

340

345

350

tgt atc cca acc tct tcc aac att gag caa caa aac tcc act cga att			1104
Cys Ile Pro Thr Ser Ser Asn Ile Glu Gln Gln Asn Ser Thr Arg Ile			
355	360	365	

cgt cag aac act aga gac cac ccc tcc acg gcc aat aca gtg gat aga			1152
Arg Gln Asn Thr Arg Asp His Pro Ser Thr Ala Asn Thr Val Asp Arg			
370	375	380	

act aat cat cag gta cgc agt ctc			1176
Thr Asn His Gln Val Arg Ser Leu			
385	390		

<210> 14
<211> 392
<212> PRT
<213> Artificial Sequence

<220>
<223> ' Opioid receptor with TEV site in 2nd
intracellular loop

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1	5	10	15
Leu Ala Tyr Ser Ser Cys Ser Pro Ala Pro Ser Pro Gly Ser Trp Val			
20	25	30	
Asn Leu Ser His Leu Asp Gly Asp Leu Ser Asp Pro Cys Gly Pro Asn			
35	40	45	
Arg Thr Asp Leu Gly Gly Arg Asp Ser Leu Cys Pro Pro Thr Gly Ser			
50	55	60	
Pro Ser Met Ile Thr Ala Ile Thr Ile Met Ala Leu Tyr Ser Ile Val			
65	70	75	80
Cys Val Val Gly Leu Phe Gly Asn Phe Leu Val Met Tyr Val Ile Val			
85	90	95	
Arg Tyr Thr Lys Met Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu			
100	105	110	
Ala Leu Ala Asp Ala Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Val			
115	120	125	
Asn Tyr Leu Met Gly Thr Trp Pro Phe Gly Thr Ile Leu Cys Lys Ile			
130	135	140	
Val Ile Ser Ile Asp Tyr Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu			
145	150	155	160
Cys Thr Met Ser Val Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys			
165	170	175	
Glu Asn Leu Tyr Phe Gln Gly Arg Asn Ala Lys Ile Ile Asn Val Cys			
180	185	190	
Asn Trp Ile Leu Ser Ser Ala Ile Gly Leu Pro Val Met Phe Ile Ala			
195	200	205	
Thr Thr Lys Tyr Arg Gln Gly Ser Ile Asp Cys Thr Leu Thr Phe Ser			
210	215	220	
His Pro Thr Trp Tyr Trp Glu Asn Leu Leu Lys Ile Cys Val Phe Ile			
225	230	235	240
Phe Ala Phe Ile Met Pro Val Leu Ile Ile Thr Val Cys Tyr Gly Leu			
245	250	255	
Met Ile Leu Arg Leu Lys Ser Val Arg Met Leu Ser Gly Ser Lys Glu			
260	265	270	

Lys Asp Arg Asn Leu Arg Arg Ile Thr Arg Met Val Leu Val Val Val
 275 280 285
 Ala Val Phe Ile Val Cys Trp Thr Pro Ile His Ile Tyr Val Ile Ile
 290 295 300
 Lys Ala Leu Val Thr Ile Pro Glu Thr Thr Phe Gln Thr Val Ser Trp
 305 310 315 320
 His Phe Cys Ile Ala Leu Gly Tyr Thr Asn Ser Cys Leu Asn Pro Val
 325 330 335
 Leu Tyr Ala Phe Leu Asp Glu Asn Phe Lys Arg Cys Phe Arg Glu Phe
 340 345 350
 Cys Ile Pro Thr Ser Ser Asn Ile Glu Gln Gln Asn Ser Thr Arg Ile
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 Arg Gln Asn Thr Arg Asp His Pro Ser Thr Ala Asn Thr Val Asp Arg
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 Thr Asn His Gln Val Arg Ser Leu
 385 390

<210> 15

<211> 1197

<212> DNA

<213> Artificial Sequence

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<223> ' Opioid receptor with TEV site in 3rd
intracellular loop

<221> CDS

<222> (1)...(1197)

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ttg gcg tac tca agt tgc tcc cca gca ccc agc ccc ggt tcc tgg gtc	96.
Leu Ala Tyr Ser Ser Cys Ser Pro Ala Pro Ser Pro Gly Ser Trp Val	
20 25 30	

aac ttg tcc cac tta gat ggc gac ctg tcc gac cca tgc ggt ccg aac	144
Asn Leu Ser His Leu Asp Gly Asp Leu Ser Asp Pro Cys Gly Pro Asn	
35 40 45	

cgc acc gac ctg ggc ggg aga gac agc ctg tgc cct cca acc ggc agt	192
Arg Thr Asp Leu Gly Gly Arg Asp Ser Leu Cys Pro Pro Thr Gly Ser	
50 55 60	

ccc tcc atg atc acg gcc atc acg atc atg gcc ctc tac tcc atc gtg	240
Pro Ser Met Ile Thr Ala Ile Thr Ile Met Ala Leu Tyr Ser Ile Val	
65 70 75 80	

tgc gtg gtg ggg ctc ttc gga aac ttc ctg gtc atg tat gtg att gtc	288
Cys Val Val Gly Leu Phe Gly Asn Phe Leu Val Met Tyr Val Ile Val	
85 90 95	

aga tac acc aag atg aag act gcc acc aac atc tac att ttc aac ctt	336
Arg Tyr Thr Lys Met Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu	
100 105 110	

gct ctg gca gat gcc tta gcc acc agt acc ctg ccc ttc cag agt gtg	384
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Ala Leu Ala Asp Ala Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Val	115	120	125	
aat tac cta atg gga aca tgg cca ttt gga acc atc ctt tgc aag ata	130	135	140	432
Asn Tyr Leu Met Gly Thr Trp Pro Phe Gly Thr Ile Leu Cys Lys Ile				
gtg atc tcc ata gat tac tat aac atg ttc acc agc ata ttc acc ctc	145	150	155	480
Val Ile Ser Ile Asp Tyr Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu				
tgc acc atg agt gtt gat cga tac att gca gtc tgc cac cct gtc aag	165	170	175	528
Cys Thr Met Ser Val Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys				
gcc tta gat ttc cgt act ccc cga aat gcc aaa att atc aat gtc tgc	180	185	190	576
Ala Leu Asp Phe Arg Thr Pro Arg Asn Ala Lys Ile Ile Asn Val Cys				
aac tgg atc ctc tct tca gcc att ggt ctt cct gta atg ttc ata gct	195	200	205	624
Asn Trp Ile Leu Ser Ser Ala Ile Gly Leu Pro Val Met Phe Ile Ala				
aca aca aaa tac agg caa ggt tcc ata gat tgt aca cta aca ttc tct	210	215	220	672
Thr Thr Lys Tyr Arg Gln Gly Ser Ile Asp Cys Thr Leu Thr Phe Ser				
cat cca acc tgg tac tgg gaa aac ctg ctg aag atc tgt gtt ttc atc	225	230	235	720
His Pro Thr Trp Tyr Trp Glu Asn Leu Leu Lys Ile Cys Val Phe Ile				
ttc gcc ttc att atg cca gtg ctc atc att acc gtc tgc tat gga ctg	245	250	255	768
Phe Ala Phe Ile Met Pro Val Leu Ile Ile Thr Val Cys Tyr Gly Leu				
atg atc ttg cgc ctc aag agt gtc cgc atg ctc tct ggc tcc aaa gaa	260	265	270	816
Met Ile Leu Arg Leu Lys Ser Val Arg Met Leu Ser Gly Ser Lys Glu				
aag gac gaa aac ctc tac ttc cag ggg agg aat ctt cga agg atc acc	275	280	285	864
Lys Asp Glu Asn Leu Tyr Phe Gln Gly Arg Asn Leu Arg Arg Ile Thr				
agg atg gtg ctg gtg gtg gct gtg ttc atc gtc tgc tgg act ccc	290	295	300	912
Arg Met Val Leu Val Val Ala Val Phe Ile Val Cys Trp Thr Pro				
att cac att tac gtc atc att aaa gcc ttg gtt aca atc cca gaa act	305	310	315	960
Ile His Ile Tyr Val Ile Ile Lys Ala Leu Val Thr Ile Pro Glu Thr				
acg ttc cag act gtt tct tgg cac ttc tgc att gct cta ggt tac aca	325	330	335	1008
Thr Phe Gln Thr Val Ser Trp His Phe Cys Ile Ala Leu Gly Tyr Thr				
aac agc tgc ctc aac cca gtc ctt tat gca ttt ctg gat gaa aac ttc	340	345	350	1056
Asn Ser Cys Leu Asn Pro Val Leu Tyr Ala Phe Leu Asp Glu Asn Phe				

aaa cga tgc ttc aga gag ttc tgt atc cca acc tct tcc aac att gag	355	360	365	1104
Lys Arg Cys Phe Arg Glu Phe Cys Ile Pro Thr Ser Ser Asn Ile Glu				
caa caa aac tcc act cga att cgt cag aac act aga gac cac ccc tcc	370	375	380	1152
Gln Gln Asn Ser Thr Arg Ile Arg Gln Asn Thr Arg Asp His Pro Ser				
acg gcc aat aca gtg gat aga act aat cat cag gta cgc agt ctc	385	390	395	1197
Thr Ala Asn Thr Val Asp Arg Thr Asn His Gln Val Arg Ser Leu				
<210> 16				
<211> 399				
<212> PRT				
<213> Artificial Sequence				
<220>				
<223> ' Opioid receptor with TEV site in 3rd				
intracellular loop				
<400> 16				
Met Asp Ser Ser Ala Ala Pro Thr Asn Ala Ser Asn Cys Thr Asp Ala	1	5	10	15
Leu Ala Tyr Ser Ser Cys Ser Pro Ala Pro Ser Pro Gly Ser Trp Val	20	25	30	
Asn Leu Ser His Leu Asp Gly Asp Leu Ser Asp Pro Cys Gly Pro Asn	35	40	45	
Arg Thr Asp Leu Gly Gly Arg Asp Ser Leu Cys Pro Pro Thr Gly Ser	50	55	60	
Pro Ser Met Ile Thr Ala Ile Thr Ile Met Ala Leu Tyr Ser Ile Val	65	70	75	80
Cys Val Val Gly Leu Phe Gly Asn Phe Leu Val Met Tyr Val Ile Val	85	90	95	
Arg Tyr Thr Lys Met Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu	100	105	110	
Ala Leu Ala Asp Ala Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Val	115	120	125	
Asn Tyr Leu Met Gly Thr Trp Pro Phe Gly Thr Ile Leu Cys Lys Ile	130	135	140	
Val Ile Ser Ile Asp Tyr Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu	145	150	155	160
Cys Thr Met Ser Val Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys	165	170	175	
Ala Leu Asp Phe Arg Thr Pro Arg Asn Ala Lys Ile Ile Asn Val Cys	180	185	190	
Asn Trp Ile Leu Ser Ser Ala Ile Gly Leu Pro Val Met Phe Ile Ala	195	200	205	
Thr Thr Lys Tyr Arg Gln Gly Ser Ile Asp Cys Thr Leu Thr Phe Ser	210	215	220	
His Pro Thr Trp Tyr Trp Glu Asn Leu Leu Lys Ile Cys Val Phe Ile	225	230	235	240
Phe Ala Phe Ile Met Pro Val Leu Ile Ile Thr Val Cys Tyr Gly Leu	245	250	255	
Met Ile Leu Arg Leu Lys Ser Val Arg Met Leu Ser Gly Ser Lys Glu	260	265	270	
Lys Asp Glu Asn Leu Tyr Phe Gln Gly Arg Asn Leu Arg Arg Ile Thr	275	280	285	

Arg Met Val Leu Val Val Ala Val Phe Ile Val Cys Trp Thr Pro
290 295 300
Ile His Ile Tyr Val Ile Ile Lys Ala Leu Val Thr Ile Pro Glu Thr
305 310 315 320
Thr Phe Gln Thr Val Ser Trp His Phe Cys Ile Ala Leu Gly Tyr Thr
325 330 335
Asn Ser Cys Leu Asn Pro Val Leu Tyr Ala Phe Leu Asp Glu Asn Phe
340 345 350
Lys Arg Cys Phe Arg Glu Phe Cys Ile Pro Thr Ser Ser Asn Ile Glu
355 360 365
Gln Gln Asn Ser Thr Arg Ile Arg Gln Asn Thr Arg Asp His Pro Ser
370 375 380
Thr Ala Asn Thr Val Asp Arg Thr Asn His Gln Val Arg Ser Leu
385 390 395

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<220>
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Cys Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
1 5 10

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Cys Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
1 5 10

<210> 19
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> enterokinase cleavage site

<400> 19
Asp Asp Asp Asp Lys
1 5

<210> 20
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<212> PRT

<213> Artificial Sequence
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<223> factor Xa cleavage site

<400> 20
Ile Glu Gly Arg
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<210> 21
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<220>
<223> thrombin cleavage site

<400> 21
Leu Val Pro Ala Gly Ser
1 5

<210> 22
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<212> PRT
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<220>
<223> renin cleavage site

<400> 22
His Pro Phe His Leu Val Ile His
1 5